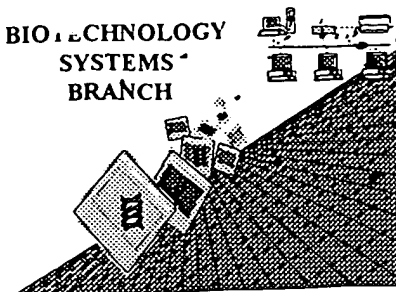


RAW SEQUENCE LISTING ERROR REPORT

BIO TECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/931,375

Source: OIPE

Date Processed by STIC: 08/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/931,375

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
 Wrapped Aminos
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
 Numbering
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
 "bug"
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
 "bug"

AMC - Biotechnology Systems Branch - 06/04/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/931,375

TIME: 17:07:12

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I931375.raw

3 <110> APPLICANT: WARMAN, Matthew L.
 4 GONG, Yaoqin
 5 OLSEN, Bjorn R.
 6 RAWADI, Georges
 7 ROMAN-ROMAN, Sergio
 9 <120> TITLE OF INVENTION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND
 THERAPY OF

Does Not Comply
Corrected Diskette Needed
See page 6 of 8A

10 OSTEOPOROSIS
 12 <130> FILE REFERENCE: 38464-0004
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/931,375
 C--> 14 <141> CURRENT FILING DATE: 2001-08-17

14 <150> PRIOR APPLICATION NUMBER: US 60/304,851

15 <151> PRIOR FILING DATE: 2001-07-13

17 <150> PRIOR APPLICATION NUMBER: US 60/234,337

18 <151> PRIOR FILING DATE: 2000-09-22

20 <150> PRIOR APPLICATION NUMBER: US 60/226,119

21 <151> PRIOR FILING DATE: 2000-08-18

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25 <170> SOFTWARE: PatentIn version 3.0

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28 <211> LENGTH: 5063

29 <212> TYPE: DNA

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39 cggctggtgg acgcggcgcg agtcaagctg gaggccacca tcgtggtcag cggcctggag	240
41 gatgcggccg cagtggactt ccagttttcc aagggagccg tgtactggac agacgtgagc	300
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RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/931,375

TIME: 17:07:12

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RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/931,375

TIME: 17:07:12

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220 Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp
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224 65 70 75 80
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227 85 90 95
229 Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly
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232 Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
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245 180 185 190
247 Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys
248 195 200 205
250 Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu
251 210 215 220
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256 Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln
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RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/931,375

TIME: 17:07:12

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Output Set: N:\CRF3\08162001\I931375.raw

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265 Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu Asp Asn Gly
266          290          295          300
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269 305          310          315          320
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272          325          330          335
274 Lys Ala Gly Ala Glu Glu Val Leu Leu Ala Arg Arg Thr Asp Leu
275          340          345          350
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278          355          360          365
280 Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu
281          370          375          380
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284 385          390          395          400
286 Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr Glu Ile Asn
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293          435          440          445
295 Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro Arg Ala Ile
296          450          455          460
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299 465          470          475          480
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302          485          490          495
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305          500          505          510
307 Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp Lys Ile Glu
308          515          520          525
310 Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu Glu Asp Lys
311          530          535          540
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314 545          550          555          560
316 Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys Val Lys Ala
317          565          570          575
319 Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met Gly Leu Lys
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322 Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys Ala Asp Arg
323          595          600          605
325 Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His Ala Thr Arg
326          610          615          620
328 Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met Lys Thr Cys
329 625          630          635          640
331 Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala Ala Ile His

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RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/931,375

TIME: 17:07:12

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Output Set: N:\CRF3\08162001\I931375.raw

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340 Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg Ala Phe Met
341          690          695          700
343 Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu Asp Tyr Pro
344 705          710          715          720
346 Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr Trp Ala Asp
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349 Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly Gln Phe Arg
350          740          745          750
352 Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser Leu Ala Leu
353          755          760          765
355 Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly Gly Lys Pro
356          770          775          780
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364 Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu Ser Ser Asn
365          820          825          830
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371          850          855          860
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374 865          870          875          880
376 Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu Val Phe His
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382 Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg Cys Gly Cys
383          915          920          925
385 Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys Ser Pro Pro
386          930          935          940
388 Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser Arg Met Ile
389 945          950          955          960
391 Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu His Gly Leu
392          965          970          975
394 Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys Phe Ile Tyr
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397 Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr
398          995          1000          1005
400 Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn Pro Asp
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Errored

09/931,375

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<210> 4
<211> 18
<212> DNA
<213> Artificial Sequence

<400> 4
ccaagtcgct tccgagac 18

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<400> 5

When the 213 response is
"Artificial Sequence" a
mandatory response is required
in field 223.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

DATE: 08/23/2001

PATENT APPLICATION: US/09/931,375

TIME: 17:07:13

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I931375.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:528 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:528 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:537 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:537 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:546 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:546 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:555 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:555 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:564 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:564 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:573 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:573 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:582 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:582 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:591 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:591 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:600 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:600 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:609 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:609 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:618 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:618 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:627 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:627 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:636 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:636 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:645 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:645 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:654 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:654 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:663 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:663 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:672 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:672 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:681 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:681 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:690 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:690 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:699 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:699 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:708 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:708 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:717 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:717 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:726 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:726 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

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L:735 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:735 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

L:744 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:744 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

L:787 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32 ✓

L:862 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40